

All glucuronosyltransferases.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 13, 2001, 12:27:19 ; Search time 78.72 Seconds
(without alignments)
509.959 Million cell updates/sec

Title: US-09-784-340-2

Sequence: 1 MRSKSLVFLLLQLFLCYGC.....KCLFSCCKFNKTRIERRE 527

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*

1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1725	61.6	528	2 JN0619	glucuronosyltransf
2	1713	61.1	530	2 A48633	glucuronosyltransf
3	1690.5	60.3	527	2 S15089	glucuronosyltransf
4	1687	60.2	529	2 A42233	glucuronosyltransf
5	1684	60.1	523	2 S11309	glucuronosyltransf
6	1676.5	59.8	528	2 A35366	glucuronosyltransf
7	1668.5	59.5	530	2 C47113	glucuronosyltransf
8	1648	58.8	531	2 B47113	glucuronosyltransf
9	1635.5	58.4	528	2 JN0620	glucuronosyltransf
10	1623.5	57.9	529	2 JN0620	glucuronosyltransf
11	1595	56.9	530	2 S68200	glucuronosyltransf
12	1577	56.3	530	2 A40467	glucuronosyltransf
13	1572	56.1	530	2 S00163	glucuronosyltransf
14	1557	55.6	530	2 A36276	glucuronosyltransf
15	1555	55.5	530	2 S07390	glucuronosyltransf
16	1137	40.6	533	2 A39092	glucuronosyltransf
17	1128.5	40.3	531	2 A35343	glucuronosyltransf
18	1109	39.6	535	2 I57961	glucuronosyltransf
19	1106.5	39.5	530	2 UC5656	glucuronosyltransf
20	1083	38.7	530	2 A55788	glucuronosyltransf
21	1078.5	38.5	530	2 S17512	glucuronosyltransf
22	1077	38.4	531	2 A31340	glucuronosyltransf
23	1052.5	37.6	529	2 A24600	glucuronosyltransf
24	1032	36.8	531	2 B55788	glucuronosyltransf
25	820.5	29.3	541	2 UC5423	2-hydroxyacylsphn
26	819	29.2	541	2 A48801	2-hydroxyacylsphn
27	735	26.2	174	2 A47113	glucuronosyltransf
28	495.5	17.7	537	2 T21823	hypothetical prote
29	491	17.5	485	2 T13694	glucuronosyltransf

30	464.5	16.6	534	2 T19944	hypothetical prote
31	453.5	16.2	531	2 T23835	hypothetical prote
32	450	16.1	508	2 T03910	UDP-glucuronosyltr
33	445	15.9	573	2 T27578	hypothetical prote
34	425.5	15.2	949	2 T18591	hypothetical prote
35	415	14.8	534	2 T19951	hypothetical prote
36	415	14.8	745	2 T23893	hypothetical prote
37	401.5	14.3	525	2 T24647	hypothetical prote
38	396.5	14.2	502	2 T25263	hypothetical prote
39	391.5	14.0	586	2 T19075	hypothetical prote
40	383.5	13.7	533	2 T34458	hypothetical prote
41	382.5	13.7	520	2 T19661	hypothetical prote
42	380	13.6	593	2 T32485	hypothetical prote
43	366	13.1	526	2 T25335	hypothetical prote
44	362.5	12.9	537	2 T25536	hypothetical prote
45	360	12.8	522	2 T31893	hypothetical prote

ALIGNMENTS

RESULT 1
JN0619
glucuronosyltransferase (EC 2.4.1.17) 2B-4 precursor - human
N:Alternate names: UDP-glucuronosyltransferase 2B-11
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jun-2000
A:Accession: JN0619; A27878
R:Jin, C.J.; Miners, J.O.; Lillywhite, K.J.; Mackenzie, P.I.
Biochem. Biophys. Res. Commun. 194, 496-503, 1993
A:Title: cDNA cloning and expression of two new members of the human liver UDP-glucur
A:Reference number: JN0619; MUID:93326164
A:Accession: JN0619
A:Molecule type: mRNA
A:Residues: 1-528 <JIN>
A:Cross-references: GB:AF081793; NID:93426331
A:Experimental source: liver
R:Jackson, M.R.; McCarthy, L.R.; Harding, D.; Wilson, S.; Coughtrie, M.W.H.; Burchell
Biochem. J. 242, 581-588, 1987
A:Title: Cloning of a human liver microsomal UDP-glucuronosyltransferase cDNA.
A:Reference number: A27878; MUID:87241362
A:Accession: A27878
A:Molecule type: mRNA
A:Residues: 1-108, 'F', 110-170, 'RP', 173-381, 'K', 383-384, 'SPR', 388-395, 'F', 397-528 <JNC
A:Cross-references: GB:Y00317; NID:937588; PIDN:CA68415.1; PID:937589
A:Genetics:
A:Gene: GDB:UGT2B4; UGT2B11
A:Cross-references: GDB:5891331; OMIM:600067
A:Map position: 4q13-4q13
C:Superfamily: glucuronosyltransferase
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase; transmembrane prot
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-528/Product: glucuronosyltransferase 2B-11 #status predicted <MET>
F:492-509/Domain: transmembrane #status predicted <TM>
F:315/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 61.6% Score 1725; DB 2: Length 528;
Best Local Similarity 62.7% Pred. No. 1.8e-128;
Matches 331; Conservative 62; Mismatches 131; Indels 4; Gaps 3;

OY 3 SDKSLVFLLLQLFLCYGC.....KCLFSCCKFNKTRIERRE 61
DB 2 SMKWTSAALLIQLSCFYSSGSGKVLVWPTFERSHMMNKITILDELVQGHETVLASSAS 61
OY 62 SLIDYRKPSALKFEVYVHMPDRTENEJFVDLALN-VLPGLSTWQSYIKLNDFFVEIRG 119
DB 62 ISFDNPSSTLKEFYVPSVLFKTEFEDIKOLVKKMAELPKDTPFWSYLSQVDEIMTFND 121
OY 120 TLKMCESFYINQTLMKLOEINIVMLIDPYIPCGDLMAELNAPFVLTIRISGMMNE 179
DB 122 ILRKCKDIVSKMKLKLQESRFDVLADAVFPGELLAEILKIPFVSLKSPGYAIE 181

QY 180 RSCGLPAPLSTYVPMVMTGLTDRMTFLERKNSMLSVLFHFWIODYHMEFEYSKALG 239
Db 182 KHSGLPFPSPYVPMVMSLSDQMTFIERKMTIYLYEFPQIFEDMKMTQFSEVIG 241
QY 240 RPTTCEYFGKAEIWLIRTYNDPEFPQIPQNFEEVGLHCKPAKALPKEMENFVSSGE 299
Db 242 RPTTSETMAKADILIRKYWDFEPHPLLPVNEFEVGGHCKPAKALPKEMEEFVSSGE 301
QY 300 DGIIVFSLGSLFQNTVEEKANITIASALAOIPQVLMRYKRGKRPSTLGANTRLYDMPOND 359
Db 302 NGVVFSLGSMVSNTESEBANYIASALAKIPQVLMRFEDGKRPDLGLNTRLYKMPOND 361
QY 360 LIGHKTKAFITHGNGNGIYEAHYHGVPMVGPVPIEGDQDNIHAKAKAAGEINEFKTMT 419
Db 362 LGHFKTKAFITHGNGNGIYEAHYHGVPMVGPVPIEGDQDNIHAKAKAAGEINEFKTMT 421
QY 420 SEDLLRALFTVITDSSYKRNARLSRIHHDQVYKPLDRAVEMIEFVMRHKAGKHLRSAH 479
Db 422 STDLLNALKTYINDPYKENMKLSRIHHDQVYKPLDRAVEMIEFVMRHKAGKHLRSAH 481
QY 480 DLTFQHSYDIVIGFLTCVATAIFLFTKCFLFCSCQKFNKTRIEKRE 527
Db 482 DLTFQHSYDIVIGFLTCVATAIFLFTKCFLFCSCQKFNKTRIEKRE 528

RESULT 2

glucuronosyltransferase (EC 2.4.1.17) precursor - human
N:Alternate names: dihydrotestosterone/androstenediol UDP-glucuronosyltransferase isoform
C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 29-Sep-1999
C:Accession: A48633; J18559
R:Chen, F.; Ritter, J.K.; Wang, M.G.; McBride, O.W.; Lubet, R.A.; Owens, I.S.
Biochemistry 32, 10648-10657, 1993
A:Title: Characterization of a cloned human dihydrotestosterone/androstenediol UDP-glucose
A:Reference number: A48633; M01D:94002056
A:Accession: A48633
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-530 <CHD>
A:Experimental source: liver
A:Note: sequence extracted from NCBI backbone (NCBIP:138786)
R:Green, M.D.; Oltur, E.M.; Tephly, T.R.
Drug Metab. Dispos. 22, 799-805, 1994
A:Title: Stable expression of a human liver UDP-glucuronosyltransferase (UGT2B15) with a
A:Reference number: J18559; M01D:95136867
A:Accession: J18559
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-530 <RES>
C:Cross-References: EMBL:U08854; NID:9475758; PIDN:AAC50077.1; PID:9475759
C:Genetics:
A:Gene: UGT2B15; UGT2B8
A:Cross-References: GDB:5692418; OMIM:600219
A:Map position: 4q13-4q13
C:Superfamily: glucuronosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 61.1%; Score 1713; DB 2; Length 530;
Best Local Similarity 62.0%; Pred. No. 1.6e-127;
Matches 327; Conservative 74; Mismatches 114; Indels 12; Gaps 5;
QY 9 VFLLLQALFC-VCCGCGKVLVPCDMSHMLNVKYLEELIYRGHEVYVLTSHKPSLIDYR 67
Db 8 VFLLLQALFCVSSGCGKVLVPMTEYSHWINKTLEELVQGHVYVLTSSASTLVNAS 67
QY 68 KPSALKFEVHMPQDRTNEENIEFDLALNVL---GLST---MQSVYKINDFEVEINGT 120
Db 68 KSSAIKLEEV-YPTSLTKND--LEDSLKILDRWYIGVSKNTFNSYFQLODELCEYDY 123
QY 121 LKMGESITVQTLMAKQIETNYDMLIDPVIPCGDLMAEALLAVFVLTLRISVGNNR 180
Db 121 LKMGESITVQTLMAKQIETNYDMLIDPVIPCGDLMAEALLAVFVLTLRISVGNNR 180

Db 124 SNKCLKDAVLNKKLMKLOESKEDVILADALNPGCELLAELEFNIPILYSLSRSVGYTEK 183
QY 181 SCGKLPAPLSTYVPMVMTGLTDRMTFLERKNSMLSVLFHFWIODYHMEFEYSKALG 240
Db 184 NGGGLFPSPYVPMVMSLSDQMTFIERKMTIYLYEFPQIFEDMKMTQFSEVIG 241
QY 241 RPTTCEYFGKAEIWLIRTYWDFEPQIPQNFEEVGLHCKPAKALPKEMENFVSSGE 300
Db 244 PTTLEETGKAEIWLIRTYWDFEPQIPQNFEEVGLHCKPAKALPKEMEEFVSSGE 303
QY 301 GIVFSLGSLFQNTVEEKANITIASALAOIPQVLMRYKRGKRPSTLGANTRLYDMPOND 360
Db 304 GIVFSLGSLGSMVSNTESEBANYIASALAKIPQVLMRFEDGKRPDLGLNTRLYKMPOND 363
QY 361 LIGHKTKAFITHGNGNGIYEAHYHGVPMVGPVPIEGDQDNIHAKAKAAGEINEFKTMT 420
Db 364 LGHFKTKAFITHGNGNGIYEAHYHGVPMVGPVPIEGDQDNIHAKAKAAGEINEFKTMT 423
QY 421 EDLLRALFTVITDSSYKRNARLSRIHHDQVYKPLDRAVEMIEFVMRHKAGKHLRSAH 480
Db 424 RDLNALKSVINDPYKENMKLSRIHHDQVYKPLDRAVEMIEFVMRHKAGKHLRSAH 483
QY 481 LTFQHSYDIVIGFLTCVATAIFLFTKCFLFCSCQKFNKTRIEKRE 527
Db 484 LTFQHSYDIVIGFLTCVATAIFLFTKCFLFCSCQKFNKTRIEKRE 530

RESULT 3

glucuronosyltransferase (EC 2.4.1.17) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C:Accession: S15089
R:Lazarov, D.; Zupko, K.; Poria, Y.; Nef, P.; Lazarovits, J.; Horn, S.; Khen, M.; Lanc
Nature 349, 790-793, 1991
A:Title: Odorant signal termination by olfactory UDP glucuronosyl transferase.
A:Reference number: S15089; M01D:91156050
A:Accession: S15089
A:Molecule type: mRNA
A:Residues: 1-527 <LAZ>
A:Cross-References: GB:X57565; NID:957762; PIDN:CAA40797.1; PID:93980217
C:Superfamily: glucuronosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 60.3%; Score 1690.5; DB 2; Length 527;
Best Local Similarity 61.5%; Pred. No. 9.4e-126;
Matches 324; Conservative 69; Mismatches 113; Indels 21; Gaps 5;
QY 13 LQFLVCGCGFCGKVLVPCDMSHMLNVKYLEELIYRGHEVYVLTSHKPSLIDYRPSAL 72
Db 10 LQSLGMSLGVNVLIMPREGSHMLNVKILIDELKEHNVYLVASGALFTTPSVPSL 69
QY 73 KFEVHMPQDRTNEENIEFDLALNVL---PGLSTWQSVK-----LNDFFVEIRGLTKMM 124
Db 70 TEIIPVPEPKIESIVKDFVLTWLENRPSTITWFKEMAKVIEEHLVSRG----I 125
QY 125 CESFIYQFLMKLOETNYDMLIDPVIPCGDLMELLAVPVVLTLRISVGNGSCGK 184
Db 126 CCGVLTAKNKLKLRQKREVLISDPVPCGDIYALKIGIPYISLRSPASTVERKCGK 185
QY 185 LPAPLSTYVPMVMTGLTDRMTFLERKNSMLSVLFHFWIODYHNF---WEEFYKALGR 240
Db 186 VFPSPYVPMVMSLSDQMTFIERKMTIYLYEFPQIFEDMKMTQFSEVIG 241
QY 241 PTTCEYFGKAEIWLIRTYWDFEPQIPQNFEEVGLHCKPAKALPKEMENFVSSGE 300
Db 241 PTTCEYFGKAEIWLIRTYWDFEPQIPQNFEEVGLHCKPAKALPKEMEEFVQTSSEH 300
QY 301 GIVFSLGSLFQNTVEEKANITIASALAOIPQVLMRYKRGKRPSTLGANTRLYDMPOND 360
Db 301 GIVFSLGSLGSMVSNTESEBANYIASALAKIPQVLMRFEDGKRPDLGLNTRLYKMPOND 360

A35366
glucuronosyltransferase (EC 2.4.1.17) UDPGln-2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 29-Sep-1999
C:Accession: A35366
R:Ritter, J.K.; Sheep, Y.Y.; Owens, I.S.
J. Biol. Chem. 265, 7900-7906, 1990
A:Title: Cloning and expression of human liver UDP-glucuronosyltransferase in COS-1 cell
A:Reference number: A35366; MUID:90243659
A:Accession: A35366
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-529 <RT>
A:Cross-references: GB:J05428; NID:9340079; PIDN:AAA6793.1; PID:9340080
C:Gene: GDB:UGT2B7; UGT2B9
A:Cross-references: GDB:5892203; OMIM:600218
A:Map position: 4q13-4q13
C:Superfamily: glucuronosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 59.8%; Score 1676.5; DB 2; Length 529;
Best Local Similarity 60.6%; Pred. No. 1.2e-124;
Matches 320; Conservative 67; Mismatches 138; Indels 3; Gaps 3;

QY 3 SDKSAVLLLLQI-FCVCGCGKVLWPCDMSHMLNVKYLEELIVRGHEVTLTHSKP 61
DB 2 SVKMTSLIQLSCFCFSSGCGKVLWMAEYSHVMNIKITLDELGRGHEVTLASSAS 61
QY 62 SLIDYKPSALKFEVYHMPDRE-ENELFVLD-ALNVLPGLSTWOSVYKLNDFEYIRG 119
DB 62 ILFDPMNSALKETIPSTLTETLENFIMQIKRMSDLPKDFMWFYFSQVQIMSIFGD 121
QY 120 TKMCESEFYIQTLMKKLOETNYDMLIDPVYPCGDMAELIAPVLTIRISVGNME 179
DB 122 ITRKFCQDVYNNKFKMKVQESRFDIAPDAIFPCSELLAELENFYVSLSPETTEE 181
QY 180 RSCGKLPAVLSVYPMVGTIDRMFLEKYNKSMLSVLFHFIQDYDYHWEFEYSKALG 239
DB 182 KNSGGEIPFSPVYVMSSELTDQMTFMEKVMNIYLVDFMFEIRDMKKMDQFYSEVIG 241
QY 240 RPTLTCEYKGAELMIRFYWDEFPQYOPNFEFVGGLHCKPAKLPKEMEFVSSGE 299
DB 242 RPTLTSETMGKADWMLIRNSMNPORPHPLLPVDFVGLHCKPAKLPKEMEFVSSGE 301
QY 300 DGIIVFSGISFQNTVEEKANITASALQIPQVLMRYKGRKPSLTGANTRLDYWIPOND 359
DB 302 NCVVVFSLGSMSNMTEERANITASALQIPQVLMRFQGNKPDILGLNTRIKKATIPOND 361
QY 360 ILGHKTRAFITNGMGNGIYEAIYHGVPMVGPPIFGDLDNTAHMKAKGAVEINFKTMT 419
DB 362 ILGHKTRAFITNGMGNGIYEAIYHGVPMVGPPIFGDLDNTAHMKAKGAARVDFNTMS 421
QY 420 SEDLLRALRTVITDSSYKENAMRLSRHHDPVKPLDRAVFIETFEVMRHKGAHLRSAAH 479
DB 422 STDLLNALKRVINDPSYKENVMKLSRHHDPVKPLDRAVFIETFEVMRHKGAHLRSAAH 481
QY 480 DLTWQHSHSIDVIGFLLCVATATFLTKCFLPSCQKFNKTRIEKRE 527
DB 482 DLTWQHSHSIDVIGFLLCVATATFLTKCFLPSCQKFNKTRIEKRE 529

RESULT 7
C47113
glucuronosyltransferase (EC 2.4.1.17) UGT2B14 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 29-Sep-1999
C:Accession: C47113
R:Tukey, R.H.; Pendurthi, U.R.; Nguyen, N.T.; Green, M.D.; Tephly, T.R.
J. Biol. Chem. 268, 15260-15266, 1993
A:Title: Cloning and characterization of rabbit liver UDP-glucuronosyltransferase cDNAs
A:Reference number: A47113; MUID:93315511

A:Accession: C47113
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-530 <TRK>
A:Cross-references: GB:L01082; NID:g165798; PIDN:AAA18020.1; PID:g165799
C:Superfamily: glucuronosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 59.5%; Score 1668.5; DB 2; Length 530;
Best Local Similarity 58.2%; Pred. No. 5.2e-124;
Matches 310; Conservative 86; Mismatches 116; Indels 21; Gaps 4;

QY 7 ALVFLLLQLQICVGC--GFCGKVLWPCDMSHMLNVKYLEELIVRGHEVTLTHSKP 63
DB 7 SVLLLLQLQISC-CFRTSGCGKVLWPMDSLMNVLVILDELVRGRHEVTLANSASIF 64
QY 64 IDYKPSALKFEVYHMPDREENEFVLDALANVLPGLSTWOSVYKLNDFEYIRG 114
DB 65 IDPSKQANIKFETFPPIATKDDLEDFVH-----VSTWTKRQNSQMKYFSLQKLP 117
QY 115 VEIRGTLKMCSEFYIQTLMKKLOETNYDMLIDPVYPCGDMAELIAPVLTIRISV 174
DB 118 SEYSDSCENACKFEVYHMPDREENEFVLDALANVLPGLSTWOSVYKLNDFEYIRG 177
QY 175 GGNMERSCGKLPAVLSVYPMVGTIDRMFLEKYNKSMLSVLFHFIQDYDYHWEFEY 234
DB 178 GYTWKTSGLSVSPSTVPTLSDLSGKMTFMEKVMNIYLVDFMFEIRDMKKMDQFY 237
QY 235 SKALGRPTLTCEYKGAELMIRFYWDEFPQYOPNFEFVGGLHCKPAKLPKEMEFV 294
DB 238 SEVLRGPRVTFSELVGRADWMLIRNSMNPORPHPLLPVDFVGLHCKPAKLPKEMEFV 297
QY 295 QSSGEGDIYVFSLSFQNTVEEKANITASALQIPQVLMRYKGRKPSLTGANTRLDYW 354
DB 298 QSSGEGGVVYVFSLSGMSNMTEERANITASALQIPQVLMRFQGNKPDILGLNTRIKK 357
QY 355 IPQNDLIGRPKTRAFITNGMGNGIYEAIYHGVPMVGPPIFGDLDNTAHMKAKGAVEIN 414
DB 358 IPQNDLIGRPKTRAFITNGMGNGIYEAIYHGVPMVGPPIFGDLDNTAHMKAKGAVEIN 417
QY 415 EKTMTSEDLLRALRTVITDSSYKENAMRLSRHHDPVKPLDRAVFIETFEVMRHKGAHL 474
DB 418 WKTMTSEDLLNALKRVINDPSYKENVMKLSRHHDPVKPLDRAVFIETFEVMRHKGAHL 477
QY 475 RGAHDLTWQHSHSIDVIGFLLCVATATFLTKCFLPSCQKFNKTRIEKRE 527
DB 478 RGAHDLTWQHSHSIDVIGFLLCVATATFLTKCFLPSCQKFNKTRIEKRE 530

RESULT 8
B47113
glucuronosyltransferase (EC 2.4.1.17) UGT2B13 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 29-Sep-1999
C:Accession: B47113
R:Tukey, R.H.; Pendurthi, U.R.; Nguyen, N.T.; Green, M.D.; Tephly, T.R.
J. Biol. Chem. 268, 15260-15266, 1993
A:Title: Cloning and characterization of rabbit liver UDP-glucuronosyltransferase cDNAs
A:Reference number: A47113; MUID:93315511
A:Accession: B47113
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-531 <TRK>
A:Cross-references: GB:L01081; NID:g165796; PIDN:AAA18020.1; PID:g165797
C:Superfamily: glucuronosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 58.8%; Score 1648; DB 2; Length 531;
Best Local Similarity 58.3%; Pred. No. 2.2e-122;
Matches 310; Conservative 84; Mismatches 120; Indels 18; Gaps 4;

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QY 7 ALVFLIQL-FCVGGCGKVLVPCDMSHMLNVKILLEILVGHVTLTHSKPSLID 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 SVLLLLQLSCSSGSGKVLVPMPEFSHMMNKITLIDLVOGHEVTLRSSASIVIG 66
QY 66 YRRPALKFEVHMPDORTENEIEFVDLALNVLEGLST---MOS-----VILNDPEV 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 SNNEGIKFEFTFHSYKXDELLENFMDYFKMIYNVSIESTWEFSLTKVILKYSIDCE 126
QY 116 EIRGTLKMCESFIYNOTLTKKLOETNYDMLIDPVIKGDLMALLAVPEVTLRLISVG 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 127 DI-----CKEYILNKKLMTKLOESRFVDLADVPSPGELLAEILLKILPLVYSLRGFEV 179
QY 176 GNNRSGCKLPAPLSYVPVMTGIDTDMTFLERKNSMLSVLFHFWIADYDHYHEEFPYS 235
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 180 YMLQKHGGGLLPSPSYVPMVSGSGSQMTFEMERQNLCLVYEDFMPKNEKMDQFYS 239
QY 236 KALGRPTLCEYKAEIWLIRTYMDEFPQYOPNFEFVGLHCKPAKALPKMENFVQ 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 240 EYLGRTVTELMGKADKMWLIRSWDEFPRLPNDFIGLGHCKRAKPLPOMEDFVQ 299
QY 296 SSGEDGIVFSLGSLFQNTVEKANIISALAOIPQKVLRYKGRKPSLGANTRLYDWT 355
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 300 SSGEEGVVPSLGSMSLNLTPEERANVIASALAPQKVLWRFEKGRKPMGSMNRLYKWI 359
QY 356 PONDILGHPKTAFTTHGNGIYEATYHGVPMGVPIFGDLDNIAHMKAKGAAYINF 415
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 360 PONDILGHPKTAFTTHGNGVFEATYHGVPIFGDLDNIAHMKAKGAAYINF 419
QY 416 KTMSEDILALRTVITDSSYKENAMRLSRHHDPVKPLDRAVFWIEFVNRHKGAKHLR 475
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 420 KTMSSADLALAKTVINDPSYKENAMRLSRHHDPVKPLDRAVFWIEFVNRHKGAKHLR 479
QY 476 SAADLTWFOHYSIDVIGFLITCVANAIFLFTKCFLESCOKFNKTRIERE 527
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 480 VAAHDLTWYOHSHIDVIGFLACVAITTYLVKCLLVRYVLGAGKRRKD 531

```

```

RESULT 9
JN0620
UDP-glucuronosyltransferase (EC 2.4.1.-) 2B-10 precursor - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-May-1999
C:Accession: JN0620
R:jin, C.J.; Miners, J.O.; Lillywhite, K.J.; Mackenzie, P.I.
Biochem. Biophys. Res. Commun. 194, 496-503, 1993
A:Title: cDNA cloning and expression of two new members of the human liver UDP-glucuronid
A:Reference number: JN0619; MUID:93326164
A:Accession: JN0620
A:Molecule type: mRNA
A:Residues: 1-528 <JIN>
A:Cross-references: GB:X63359; NID:9516149; PIDN:CA44961.1; PID:9516150
A:Experimental source: Liver
C:Superfamily: glucuronosyltransferase
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <Sig>
F:24-528/Product: UDP-glucuronosyltransferase 2B-10 #status predicted <MET>
F:491-508/Domain: transmembrane #status predicted <TM>
F:66/314/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

```

Query Match 58.4%; Score 1635.5; DB 2; Length 528;
Best Local Similarity 59.8%; Pred. No. 2.1e-121;
Matches 311; Conservative 72; Mismatches 134; Indels 3; Gaps 2;

```

```

QY 11 LLLQL-FCVGGCGKVLVPCDMSHMLNVKILLEILVGHVTLTHSKPSLIDYRK 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 9 LLLQLSFYSSGSGKVLVMAAEYSLMMNKITLKEIVQGHETVYLASSASILFDRNDS 68
QY 70 SALKFEVHMPDORTENEIEFVDL-LNVLPGLSTQSVIKLNDPVEILRGTLKMCES 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 69 STLKLEVPYSLTKTEFENIMQVLRKLSIQKDTFVLPSQGEILMALINDIRNCKD 128
QY 128 FIYNOTLTKKLOETNYDMLIDPVIKGDLMALLAVPEVTLRLISVGNNRSGCKLPA 187

```

```

Db 129 VSNKKLTKKLOESRFDIVADAVLPCGELLAEFLNIPFYSHSFSGYSPERSGCFIF 188
QY 188 PLSTVYPMTGLDRTMTFLERKNSMLSVLFHFWIADYDHYHEEFPYSKALGRPTLCE 247
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 189 PPSVVPVPMKLSQMTFEMERQNLCLVYEDFMPKNEKMDQFYS 248
QY 248 VGRKAEIWLIRTYMDEFPQYOPNFEFVGLHCKPAKALPKMENFVQSGEDGIVFSL 307
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 249 MKRADIMLNRNSMFKRPHFPLPVNDFVGGIHCAPKPLKREMEEFVQSGENGCVVFS 308
QY 308 GSLFQNTVEKANIISALAOIPQKVLRYKGRKPSLGANTRLYDWTGHPKTR 367
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 309 GSNVSNMTEERANVIASALAPQKVLWRFEKGRKPMGSMNRLYKWI 368
QY 368 AFTHGNGIYEATYHGVPMGVPIFGDLDNIAHMKAKGAAYINFKTMSEDILAL 427
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 369 AFTHGANGIYEATYHGVPIFGDLDNIAHMKAKGAAYINFKTMSEDILAL 428
QY 428 RTVITDSSYKENAMRLSRHHDPVKPLDRAVFWIEFVNRHKGAKHLRSAADLTWFOHY 487
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 429 KTVINDPSYKENIKLSRIHDPVKPLDRAVFWIEFVNRHKGAKHLRVAHNLTFWOYH 488
QY 488 SIQVIGFLITCVANAIFLFTKCFLESCOKFNKTRIERE 527
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 489 SLQVIGFLITCVANAIFLFTKCFLESCOKFNKTRIERE 528

```

```

RESULT 10
JE0200
orphan UDP-glucuronosyltransferase (EC 2.4.-.-) - human
N:Alternate names: UGT2B11
C:Species: Homo sapiens (man)
C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
C:Accession: JE0200
R:Beaulieu, M.; Levesque, E.W.; Hum, D.; Belanger, A.
Biochem. Biophys. Res. Commun. 248, 44-50, 1998
A:Title: Isolation and characterization of a human orphan UDP-glucuronosyltransferase
A:Reference number: JE0200; MUID:98340847
A:Accession: JE0200
A:Molecule type: mRNA
A:Residues: 1-529 <BEA>
A:Cross-references: GB:AF016492
C:Comment: This enzyme catalyzes the transfer of glucuronic acid to a wide range of e
C:Superfamily: glucuronosyltransferase
C:Keywords: glycoprotein; glycosyltransferase
F:493-509/Domain: membrane-anchoring #status predicted <MAC>
F:315/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

```

Query Match 57.9%; Score 1623.5; DB 2; Length 529;
Best Local Similarity 58.7%; Pred. No. 1.9e-120;
Matches 311; Conservative 71; Mismatches 129; Indels 19; Gaps 4;

```

```

QY 9 VELLQLFC-VGGCGKVLVPCDMSHMLNVKILLEILVGHVTLTHSKPSLIDYR 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 VLLIHLISCYFSSGSGKVLVMAAEYSHMMNKITLKEIVQGHETVYLASSASILFDPN 67
QY 68 KPSALKFEVHMPDORTENEIEFVDLALNVLPGLSTQSVIKLNDPVE-----EI 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 DASLTKFEVPTSLTKTEFENI-----IMQYKRN-SDIRKSFMLYSQDEIIMEL 119
QY 118 RGLTKMCCESFIYNOTLTKKLOETNYDMLIDPVIKGDLMALLAVPEVTLRLISVGN 177
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 120 YDIPRNCKDVNSKKYMKKLOESRFDIVADAVPCGELLALALNIRFYSLFTPGYT 179
QY 178 MESSCGLPAPLSYVPVMTGIDRTMTFLERKNSMLSVLFHFWIADYDHYHEEFPYSKA 237
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 180 IERRSGGLIPPSYIPYIMSKLSQMTFEMERQNLCLVYEDFMPKNEKMDQFYS 239
QY 238 LGRPTLCEYKAEIWLIRTYMDEFPQYOPNFEFVGLHCKPAKALPKMENFVQSS 297
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 240 LGRPTLCEYKAEIWLIRTYMDEFPQYOPNFEFVGLHCKPAKALPKMENFVQSS 299

```

```

OY 298 GBDGIVFSLGSLFQVTEEEKANIISALAOIPQKVLNRYKGGKPPSTLGANTRLYMIQ 357
    ||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 300 GENGVAVFSLGVSVMTEBRANVITAKIPQKVLNRYKGGKPPSTLGANTRLYMIQ 359
OY 358 NDLLGPKTKAFITTHGGANGIYEALYHGVPMVGPPIFGQDLNIAHMKAGAAVEINFTK 417
    |||||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 360 NDLLGPKTKAFITTHGGANGIYEALYHGVPMVGPPIFGQDLNIAHMKAGAAVEINFTK 419
OY 418 MTSDDLRLALRTVITDSSYKEMANRLSRTHHDQPKPLDRAVFWIEFWVRHKGAAHLSA 477
    ||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 420 MTSDDLRLALRTVITDSSYKEMANRLSRTHHDQPKPLDRAVFWIEFWVRHKGAAHLSA 479
OY 478 AHDLTWPHYSIDVIGFLLTCVATAIFLTKCFPLSCOKFNKTRIKRE 527
    |||||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 480 AHDLTWPHYSIDVIGFLLTCVATAIFLTKCFPLSCOKFNKTRIKRE 529

```

RESULT 11

```

S68200
glucuronosyltransferase (EC 2.4.1.17) precursor - rat
N:Alternate names: UDP-glucuronosyltransferase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
C:Accession: S68200; A61266
R:Green, M.D.; Clarke, D.J.; Ocuru, E.M.; Styczynski, P.B.; Jackson, M.R.; Burchell, B.;
Arch. Biochem. Biophys. 322, 460-468, 1995
A:Title: Cloning and expression of a rat liver phenobarbital-inducible UDP-glucuronosylt
A:Reference number: S68200; MUID:96032669
A:Accession: S68200
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-530 <GRE>
A:Cross-references: EMBL:U06273; NID:9458394; PID:AAA83404.1; PID:9458395
R:Styczynski, P.; Green, M.; Pulig, J.; Coffman, B.; Tephly, T.
Mol. Pharmacol. 40, 80-84, 1991
A:Title: Purification and properties of a rat liver phenobarbital-inducible 4-hydroxybip
A:Reference number: A61266; MUID:91312327
A:Accession: A61266
A:Status: preliminary
A:Molecule type: protein
A:Residues: 24-36 <STY>
C:Superfamily: glucuronosyltransferase
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-530/Product: glucuronosyltransferase #status predicted <MAT>

```

```

Query Match          56.9%; Score 1595; DB 2; Length 530;
Best Local Similarity 57.9%; Pred. No. 3,3e-118;
Matches 307; Conservative 74; Mismatches 143; Indels 6; Gaps 3;

```

```

OY 3 SDRSALVFLLILOT-FCVGGGFCGKVLVPCDMSHMLNVAVILBELIVRGHEVTVLTHSKP 61
    |||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 2 SGWMAIALLLILQISFCFKSGNCGKVLVPMDEYSHMNKILILELQOKGHEVTVLTPSAF 61
OY 62 SLIDYRPSALKEFVYVHMDPDRTEENIEFVDALAN-----LPLSTWQSVYIKNDFFVEL 117
    ||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 62 VFELDPKETSDLKF-VTFPTSESSHDELENFTFRVNVNWTLELPDITGLSTFLYIADITDEX 120
OY 118 RGTLMKMCSEFIYNTLAKKLOETNYDVLIDPVIIPCGDLMAELLAVPVLRLTSVGN 177
    ||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 121 SDYCLTVCKEAVSNQFMKQLQESKEDVFSDAIGCGELIAELLQIPLYLSRSPGYT 180
OY 178 MRSQGLKLPAPLSYVPVPMTGLDRMTFLERVKNSMLSVLFHFVIODYVHWEERYSA 237
    ||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 181 IEDYIGVAFPPSYPMFISGLAGQMTFLERVHNMCMLYEFDFWQTFEKKWDPFYSKT 240
OY 238 ICRPTTLCEYGAKEIWLIRIYWDEFPQYQNFEEVGLCKCPAKAPKEMENVOSS 297
    |||||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 241 IGRPTTLAEIMKAKEMMILRSYWDLEFPHPISPNDYIGGLCKCPAKPLPKRIEDFVOSS 300
OY 298 GBDGIVFSLGSLFQVTEEEKANIISALAOIPQKVLNRYKGGKPPSTLGANTRLYMIQ 357

```

```

Db 301 GENGVAVFSLGVSVMTEEEKANIISALAOIPQKVLNRYKGGKPPSTLGANTRLYMIQ 360
OY 358 NDLLGPKTKAFITTHGGANGIYEALYHGVPMVGPPIFGQDLNIAHMKAGAAVEINFTK 417
    |||||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 361 NDLLGPKTKAFITTHGGANGIYEALYHGVPMVGPPIFGQDLNIAHMKAGAAVEINFTK 420
OY 418 MTSDDLRLALRTVITDSSYKEMANRLSRTHHDQPKPLDRAVFWIEFWVRHKGAAHLSA 477
    ||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 421 MTSDDLRLALRTVITDSSYKEMANRLSRTHHDQPKPLDRAVFWIEFWVRHKGAAHLSA 480
OY 478 AHDLTWPHYSIDVIGFLLTCVATAIFLTKCFPLSCOKFNKTRIKRE 527
    |||||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 481 AHDLTWPHYSIDVIGFLLTCVATAIFLTKCFPLSCOKFNKTRIKRE 530

```

RESULT 12

```

A40467
glucuronosyltransferase (EC 2.4.1.17) precursor - rat
N:Alternate names: UDP-glucuronosyltransferase isoform 53K
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Feb-1992 #sequence_revision 07-Feb-1992 #text_change 17-Nov-2000
C:Accession: A40467; A23520; S59627; A26064; I55247
R:Haque, S.J.; Petersen, D.D.; Nebert, D.W.; Mackenzie, P.I.
DNA Cell Biol. 10, 515-524, 1991
A:Title: Isolation, sequence, and developmental expression of rat UGT2B2: the gene en
A:Reference number: A40467; MUID:91369480
A:Accession: A40467
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-530 <RHO>
R:Jackson, M.R.; Burchell, B.
Nucleic Acids Res. 14, 779-795, 1986
A:Title: The full length coding sequence of rat liver androsterone UDP-glucuronyltran
A:Reference number: A23520; MUID:86120371
A:Accession: A23520
A:Molecule type: mRNA
A:Residues: 31-158,'E',160-285,'S',287-350,'T',352-362,'T',364-430,'E',432-530 <JAC>
A:Cross-references: GB:X03478; NID:957452; PID:CAA27198.1; PID:957453
R:Note: the authors translated the codon ATT for residue 321 as Asn
R:Yamashita, A.; Watanabe, M.; Tonegawa, T.; Sugitara, T.; Waku, K.
Biochem. J. 312, 301-308, 1995
A:Title: Acyl-CoA binding and acylation of UDP-glucuronosyltransferase isoforms of ra
A:Reference number: S59627; MUID:96077159
A:Accession: S59627
A:Molecule type: protein
A:Residues: 24-44 <YAM>
R:Mackenzie, P.I.
J. Biol. Chem. 261, 14112-14117, 1986
A:Title: Rat liver UDP-glucuronosyltransferase: cDNA sequence and expression of a for
A:Reference number: A26064; MUID:87033594
A:Accession: A26064
A:Molecule type: mRNA
A:Residues: 1-430,'E',432-530 <MAC>
A:Cross-references: GB:J02589; NID:9207582; PID:AAA42314.1; PID:9207583
R:Experimental source: hepatic
C:Superfamily: glucuronosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-530/Product: glucuronosyltransferase #status experimental <MAT>

```

```

Query Match          56.3%; Score 1577; DB 2; Length 530;
Best Local Similarity 56.4%; Pred. No. 8.9e-117;
Matches 301; Conservative 74; Mismatches 137; Indels 22; Gaps 4;

```

```

OY 6 SALVFLLIQLFCVGGGFCGKVLVPCDMSHMLNVAVILBELIVRGHEVTVLTHSKP 65
    |||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 7 SALVFLDQISYFCFKSGHCGKVLVPMDEYSHMNKILILELQOKGHEVTVLTPSAF 65
OY 66 YRKPALKFVYVHMDPDRTEENIEFV-----DLANLVYVPGSTWQSVYIKNDF 113
    |||||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 66 PKSSDLKFEIRSTISIDELQNHFIKLLDWTYELPDTGLSTSPITQ--NLVTEESTF 123

```

OY 114 FVEIRGTLKMGESFIYNOTLTKKLOETNYDMLIDPVIIPCGDLMALLAEPVLTIRIS 173
DB 124 YLST-----CKDAVSNKQMLTKLOESKFVLPADPVASGDLIAELLHIPPVLSLSES 176
OY 174 VGGNMRSCGKLPAPLSYVPVPMGTGLTDRMTFLERKNSMLVLPFHFIODDYHFMEEF 233
DB 177 PGRHKLEKSGKILPSPYVPLISGLAGKMTFIDRYKNNMICMLYDFEWEERLRHKEMDFF 236
OY 234 YSKALGPTTLCETVGAKEIMLIRTYWDEFPQYOPNEFVGLCHCKPAKALPKEMENF 293
DB 237 YSEILGRPTVDETMSKVEIMLIRSYWDLKFPHPPLPNVDYIGGLHCKPAKPLPKDMEEF 296
OY 294 VOSSDEGIVVTSLSLQONTVEEKANITASALAOIPQVLMRYKRGKRSSTIGANTRLUD 353
DB 297 VOSSGEHGVVTSLSMSVNMTEEKANALAMALAOIPQVLMKFPDKTPATLGGKPNRYK 356
OY 354 WIPQDGLGHPRTKAFITGHGNGIYEALYHGVPMVGPPIFGDQDNIAMHAKGAIVEI 413
DB 357 WIPQDGLGHPRTKAFITGHGNGIYEALYHGVPMVGPPIFGDQDNIAMHAKGAIVEI 416
OY 414 NEKMTSEDLALRTVITDSSYKENAMRLSRIHNDQVPKPLDRAVFWIEFWRHGAKH 473
DB 417 NRTMSKIDFLSALVEYIDNPYKKVMLSTIHDQPKPLDRAVFWIEFWIRHAKH 476
OY 474 LRSAHDLTWPHYSIDVIGFLITCVATRIEFTKCFLESCOKFKTRIEKR 527
DB 477 LRLIGHNLPMVOYHSLDIVIGFLITCFVATLALTVKCLFMRYEFREKKEKRN 530

RESULT 13

glucuronosyltransferase (EC 2.4.1.17) precursor - mouse
N:Alternate names: UDP-glucuronosyltransferase
C:Species: Mus musculus (house mouse)
C:Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 29-Sep-1999
C:Accession: S00163
R:Kimura, T.; Owens, I.S.
Eur. J. Biochem. 168, 515-521, 1987
A:Title: Mouse UDP-glucuronosyltransferase. cDNA and complete amino acid sequence and re
A:Reference number: S00163; MUID:88029469
A:Accession: S00163
A:Molecule type: mRNA
A:Residues: 1-530 <KIN>
A:Cross-references: EMBL:X06358; NID:955119; PIDN:CAA29657.1; PID:955120
C:Comment: This enzyme catalyzes the conjugation of lipophilic compounds with glucuronic
C:Superfamily: glucuronosyltransferase
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase; transmembrane protein
F:1-16/Domain: signal sequence #status predicted <STIG>
F:17-530/Product: glucuronosyltransferase #status predicted <MTM>
F:494-510/Domain: transmembrane #status predicted <TM>
F:316,483/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.1%; Score 1572; DB 2; Length 530;

Best Local Similarity 56.2%; Pred. No. 2.2e-116;

Matches 304; Conservative 86; Mismatches 115; Indels 36; Gaps 8;

OY 6 SALVFLLLQLFCVGGCF---CGKVLWPCDMSHMLNVKVLIELIVRGHEVTVLTHSKP 61
DB 7 SALVFLLLQLFCVGGCF---CGKVLWPCDMSHMLNVKVLIELIVRGHEVTVLTHSKP 61
OY 62 SLIDYRKPSALKFEVYVHMPDRTEEN-----EIFVDLALVGLSTQSY 107
DB 62 YLDPKPSGKLFET--PFTSVSKONLENFIFKFDVWVWYEMPRDCLSYPL--QNM 116
OY 108 I-KLNDPVEIRIGTLKMGESFIYNOTLTKKLOETNYDMLIDPVIIPCGDLMALLAEPV 166
DB 117 IDEFSDYFLS-----LCKDVVSNKEILMTKLOESKFVLPADPVASGDLIAELLHIPP 169
OY 167 VTLTISVGGNMRSCGKLPAPLSYVPVPMGTGLTDRMTFLERKNSMLVLPFHFIODDY 226
DB 170 LYSIRFSFGYQIEKSSGRLPLPSPYVPLISGLGGMFTIERIKNNICMLYDFEWEER 229

OY 227 YHFMEEFYKALGRPTTLCETVGAKEIMLIRTYWDEFPQYOPNEFVGLCHCKPAKAL 286
DB 230 DKRWDSFYSEYGLRPTTLCETVGAKEIMLIRTYWDEFPQYOPNEFVGLCHCKPAKAL 289
OY 287 PKEMENFVOSSGEGDGLVTSLSLQONTVEEKANITASALAOIPQVLMRYKRGKRSSTIG 346
DB 290 PKDMEFVOSSGEGDGLVTSLSLQONTVEEKANITASALAOIPQVLMRYKRGKRSSTIG 349
OY 347 ANTRLDWIPQDGLGHPRTKAFITGHGNGIYEALYHGVPMVGPPIFGDQDNIAMHAK 406
DB 350 HNTRVYKMLPQDGLGHPRTKAFITGHGNGIYEALYHGVPMVGPPIFGDQDNIAMHAK 409
OY 407 KGAALVINKRTMTSEDLALRTVITDSSYKENAMRLSRIHNDQVPKPLDRAVFWIEFW 466
DB 410 KGAALVINKRTMTSEDLALRTVITDSSYKENAMRLSRIHNDQVPKPLDRAVFWIEFW 469
OY 467 RHGAKHLRSAHDLTWPHYSIDVIGFLITCVATRIEFTKCFLESCOKFKTRIEKR 526
DB 470 RHGAKHLRPLGHNLTYOYHSLDIVIGFLITCVATRIEFTKCFLESCOKFKTRIEKR 529
OY 527 E 527
DB 530 E 530

RESULT 14

A36276
glucuronosyltransferase (EC 2.4.1.17) 5 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 18-Jan-1991 #sequence_revision 13-Jan-1993 #text_change 29-Sep-1999

C:Accession: A36276

R:MacKenzie, P.I.
J. Biol. Chem. 265, 8699-8703, 1990

A:Title: The cDNA sequence and expression of a variant 17beta-hydroxysteroid UDP-gluc

A:Reference number: A36276; MUID:90256795

A:Accession: A36276

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-530 <MAC>

A:Cross-references: GB:M33746; GB:J05440; NID:9207570; PIDN:AAA03217.1; PID:9207572

A:Note: the authors translated the codon GAG for residue 530 as Lys

C:Superfamily: glucuronosyltransferase

C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 55.6%; Score 1557; DB 2; Length 530;

Best Local Similarity 54.5%; Pred. No. 3.4e-115;

Matches 292; Conservative 90; Mismatches 132; Indels 22; Gaps 4;

OY 5 KSAVFLLLQLFCVGGCF---CGKVLWPCDMSHMLNVKVLIELIVRGHEVTVLTHSKP 63
DB 4 KMFALLLLQISFLCSAKCGKVLWPMFESHMNNIKTILDELVOGRHEVTVLTPSAVYV 63
OY 64 IDYRKPSALKFEVYVHMPDRTEENEIFVDA-----LNVPLGLSTQSYIKLN 111
DB 64 LDPKSPDILQIFSPCLRSAGCGKVLWPMFESHMNNIKTILDELVOGRHEVTVLTPSAVYV 63
OY 112 DPEVETRGTLKMGESFIYNOTLTKKLOETNYDMLIDPVIIPCGDLMALLAEPVLTIR 171
DB 122 DYLLSV-----CKDAVSNKQMLTKLOESKFVLPADPVASGDLIAELLHIPPVLS 174
OY 172 ISVGNMRSCGKLPAPLSYVPVPMGTGLTDRMTFLERKNSMLVLPFHFIODDYHFM 231
DB 175 ASGDKHIEKSSGRLPLPSPYVPLISGLGGMFTIERIKNNICMLYDFEWEERLHAK 234
OY 232 EYYSKALGPTTLCETVGAKEIMLIRTYWDEFPQYOPNEFVGLCHCKPAKALPKEME 291
DB 235 PYTELIGRPTTLCETVGAKEIMLIRTYWDEFPQYOPNEFVGLCHCKPAKALPKEME 294
OY 292 NTVOSGEGDGLVTSLSLQONTVEEKANITASALAOIPQVLMRYKRGKRSSTIGANTRL 351
DB 295 DTVOSGEGDGLVTSLSLQONTVEEKANITASALAOIPQVLMRYKRGKRSSTIGANTRL 354

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